

[illegible][illegible]

Figure 2A  
Interleukin-22

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1  GGAATTTCGGCACGAGCTCGTGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGC 60
1  N S A R A R A V L S A F H H T L Q L G P 20

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61  CGCGTGAGCAGGCGCGCAACGCGAGCTGCCCGGCAGGGGGCAGGCCCGCCGACCGCCGCT 120
21  R E Q A R N A S C P A G G R P A D R R F 40

121  TCCGGCCGCCCACCAACCTGCGCAGCGTGTGCGCCCTGGGCCTACAGAATCTCCTACGACC 180
41  R P P T N L R S V S P W A Y R I S Y D P 60
                                     Domain I

181  CGGCGAGGTACCCACAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCG 240
61  A R Y P R Y L P E A Y C L C R G C L T G 80
      Domain I                      Domain II

241  GGCTGTTTCGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCTGTCTACATGCCACCGTGC 300
81  L F G E E D V R F R S A P V Y M P T V V 100
                                     Domain III

301  TCCTGCGCCGCACCCCGCCTGCGCCGGCGCCCGTTCGCTCTACACCGAGGCCTACGTCA 360
101  L R R T P A C A G G R S V Y T E A Y V T 120
      Domain III

#

361  CCATCCCCGTGGGCTGCACCTGCGTCCCCGAGCCGGAAGAAGACGCAGACAGCATCAACT 420
121  I P V G C T C V P E P E K D A D S I N S 140
      Domain IV

421  CCAGCATCGACAAACAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCC 480
141  S I D K Q G A K L L L G P N D A P A G P 160

481  CCTGAGGCCGGTCTCTGCCCGGGAGGTCTCCCGGCCCGCATCCCGAGGCGCCCAAGCTG 540

541  GAGCCGCTTGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGACCCGAGCAAACCAAGTG 600

601  CCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCA 660

661  TCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACC 720

721  CGGCACGGGCATCCTGTGTGCGGCCCGCATGGAGGGTTTGGAAGTTTACGGAGGCTCC 780

781  CTGAGGAGCCTCTCAGATCGGCTGCTGCGGGTGCAGGGCGTGACTACCGCTGGGTGCTT 840

841  GCCAAAGAGATAGGGACGCATATGCTTTTTAAAGCAATCTAAAAATAATAAAGTATAG 900

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CCDS: E22220

Figure 2B  
Interleukin-22

901 CGACTATATACCTACTTTTAAAATCAACTGTTTGAATAGAGGCAGAGCTATTTTATATT 960  
961 ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTTACTTCTTC 1020  
1021 TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTGTAGCTGGTACACTC 1080  
1081 TGGCCTGGGTCTCTGAATTCAGCCTGTCCCGATGGCTGACTGATGAAATGGACACGTCT 1140  
1141 CATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG 1200  
1201 ATGCACAGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGG 1260  
1261 TTTTAGTCATGAATACATAAACAGTCTCAAACCTGCACAATTTTTTCCCCCTTTTGAAAG 1320  
1321 CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGAACGTGACATCTTT 1380  
1381 GCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG 1440  
1441 CTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT 1500  
1501 GTTCTGCAATCTGCCACGAGAGCTAGGTCTTGATCTTTTCTTTAGATTGAAAGTCTGT 1560  
1561 CTCTGAACACAATTATTTGTAAAAGTTAGTAGTTCTTTTAAATCATTAAAAGAGGCTT 1620  
1621 GCTGAAAAAAAAAAAAAAAAAAAA 1642



	110	120	130	140	150	
67	- - - - -	Y N R S T S P W	N L H R N E D P E R Y P S V	I W E A K C R H L G C C I N A D - G N V D Y	IL-17.aa	
70	- - - - -	L N R S T S P W	T L H R N E D P D R Y P S V	I W E A Q C R H Q R C V N A E - G K L D H	mIL-17.aa	
63	- - - - -	Y N R S T S P W	T L H R N E D Q D R Y P S V	I W E A K C R Y L G C V N A D - G N V D Y	vIL-17.aa	
88	L Q L W M S N K	- R S L S P W	G Y S I N H D P S R I P V D L L A F A E C L C R G C C I D A R T G R E T A	P F T M Q E D R	IL20.aa	
2	- - - - -	- - - - -	- - - - -	- - - - -	IL-21.aa	
96	V - L E A D T H Q R S I S P W R Y R V D T D E D R Y P Q K L A F A E C L C R G C C I D A R T G R E T A	- - - - -	- - - - -	- - - - -	IL21FL.aa	
91	R R F R P P T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y C L C R G C C L T G L F G E E D V	- - - - -	- - - - -	- - - - -	IL-22.aa	
91	R R F R P P T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y C L C R G C C L T G L F G E E D V	- - - - -	- - - - -	- - - - -	IL22ext.aa	

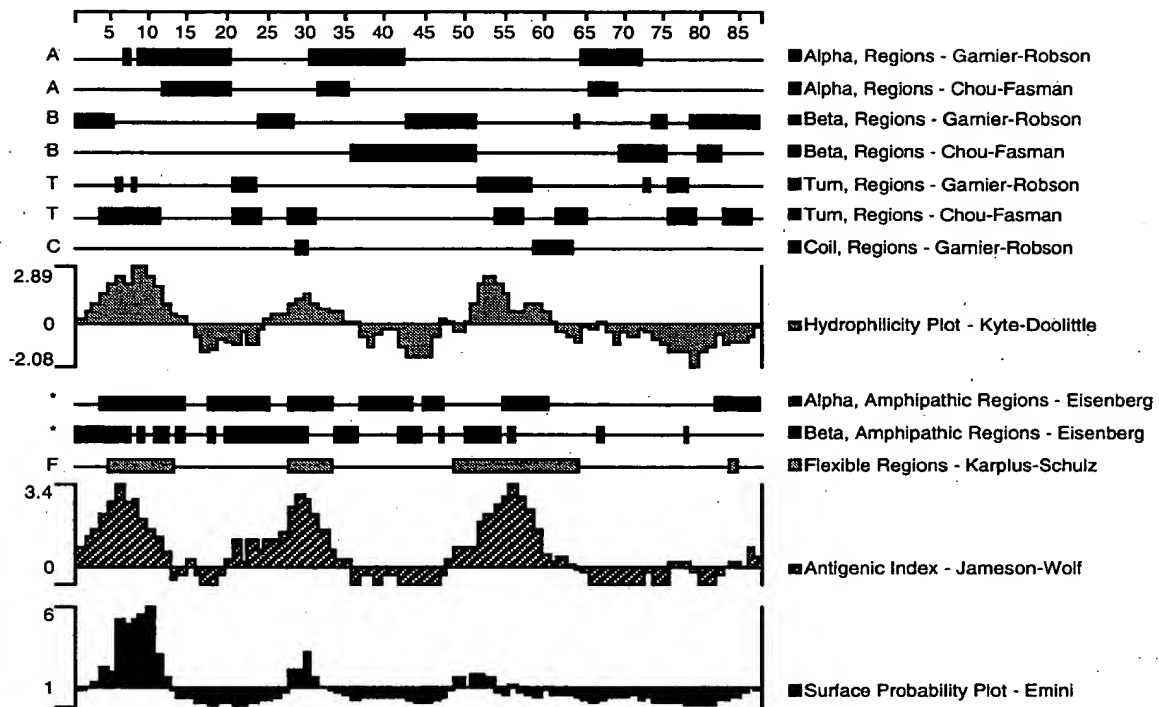
	160	170	180	190	200	
109	H M N S V P I Q Q Q E I L V L R R E P - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	IL-17.aa
112	H M N S V L I Q Q Q E I L V L K R E P - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	mIL-17.aa
105	H M N S V P I Q Q Q E I L V V R K G H - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	vIL-17.aa
137	S M V S V P V F - S Q V P V R R R L C P P P R T G P C R Q - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	IL20.aa
35	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	IL-21.aa
145	A L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	IL21FL.aa
88	R F R S A P V Y M P T V L R R T P A C A G G R S V - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	IL-22.aa
101	R F R S A P V Y M P T V L R R T P A C A G G R S V - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	IL22ext.aa

Figure 3B

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**Figure 4**  
**Interleukin-21 Polypeptide Analysis**



**Figure 5**  
**Interleukin-22 Polypeptide Analysis**

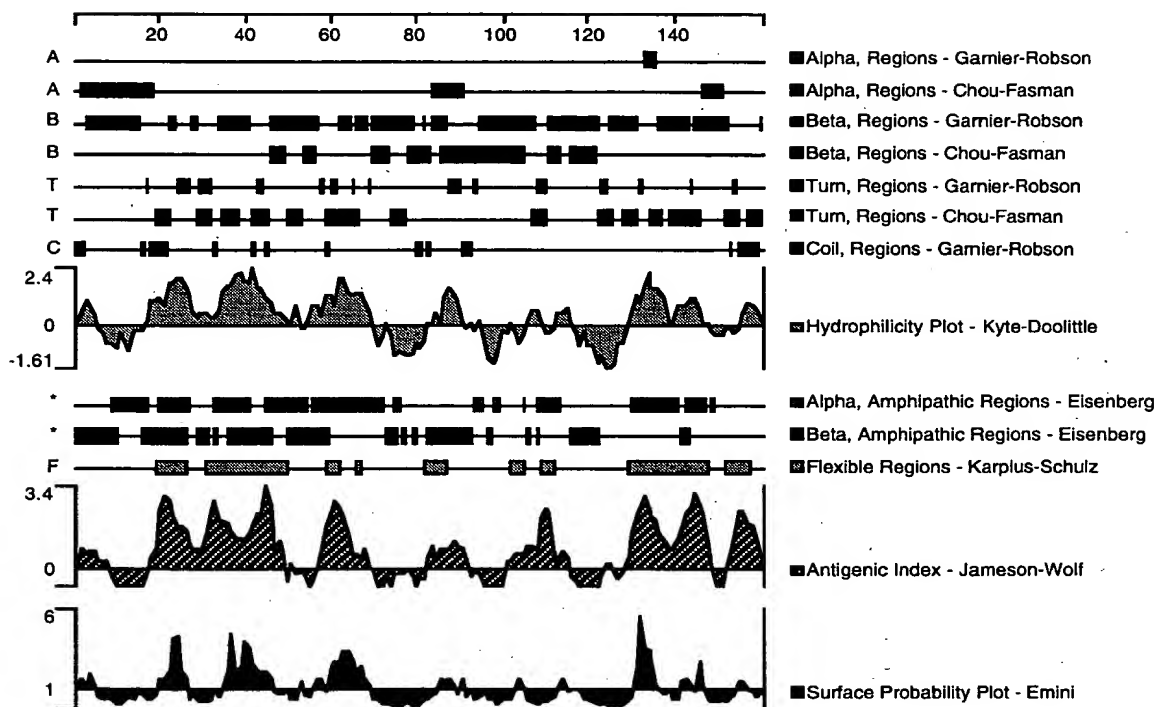




Figure 6A  
Interleukin-21

1	GCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTGTT	60
1	<u>M T L L P G L L F</u>	9
61	CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC	120
10	<u>L T W L H T C L A</u> H H D P S L R G H P H	29
121	AGTCACGGTACCCCACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGCCCCCCCA	180
30	S H G T <u>P H C Y S A E</u> E L P L G Q A P P	49
	Domain V	
181	CACCTGCTGGCTCGAGGTGCCAAGTGGGGGAGGCTTTGCCTGTAGCCCTGGTGTCCAGC	240
50	H L L A R G A K W G Q A L <u>P V A L V S S</u>	69
	Domain VI	
241	CTGGAGGCAGCAAGCCACAGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG	300
70	L E A A S H R G R H E R P S A T T Q C P	89
301	GTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACCCACCAGCGCTCCATCTCACCCCTGG	360
90	V L R P E E V L E A D T H Q <u>R S I S P W</u>	109
	Domain VII	
361	AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC	420
110	R Y R <u>V D T D E D R Y P</u> Q K L A F A E C	129
	Domain I	Domain II
421	CTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG	480
130	<u>L C R G C</u> I D A R T G R E T A A L N S V	149
	Domain II	
481	CGGTGCTCCAGAGCCTGCTGGTGCTGCGCCCGCGGCCCTGCTCCCGCGACGGCTCGGGG	540
150	R L L Q S L <u>L V L R R R P</u> C S R D G S G	169
	Domain III	
541	CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTTCATCCACGTCCCCGTCGGCTGC	600
170	L P T P G A F A F H T E F I H <u>V P V G C</u>	189
	Domain IV	
601	ACCTGCGTGCTGCCCCGTTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC	660
190	<u>T C V</u> L P R S V	197
	Domain IV	
661	GTGTGCTCCCCAGAGGGCACCCCTATTTATGTGTATTTATGTATTTATATGCCTCCC	720
721	CCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTC	780

**Figure 6B**  
**Interleukin-21**

781 TCCTCATCTCCAGCCTCAGTAGTTGGGGGTWGAAGGAGCTCAGCACCTCTTCCAGCCCTT 840  
841 AAAGCTGCAGAAAAGGTGTACACGGCTGCCTGTACCTTGGYTCCCTGTCTGCTCCCGG 900  
901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960  
961 GAAGTACCCTGTTTCTTAACAATTATTTAAGTGACGTGTATTATTAAACTGATGAAC 1020  
1021 ACAA 1067

20250226

**Figure 7**  
**Interleukin-21 Polypeptide Analysis**

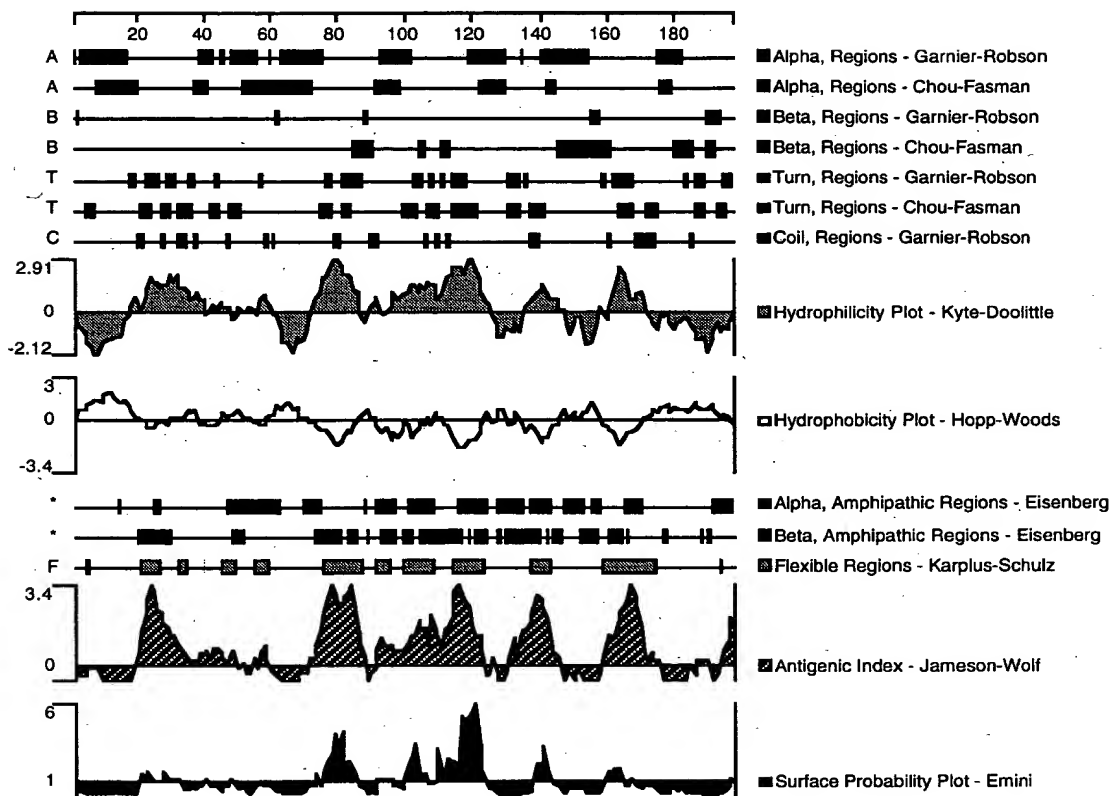


Figure 8  
Interleukin-22

1	GGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCCGCG	60
1	G C A D R P E E L L E Q L Y G R L <u>A A G</u>	20
	CD-VI	
	#	
61	GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCG	120
21	<u>V L S</u> A F H H T L Q L G P R E Q A R N A	40
	CD-VI	
121	AGCTGCCCCGCGAGGGGGCAGGCCCGCCGACCGCCGCTTCCGGCCGCCACCAACCTGCGC	180
41	S C P A G G R P A D R R F R P P T N L <u>R</u>	60
181	AGCGTGTCGCCCTGGGCCTACAGAATCTCCTACGACCGGCGAGGTACCCAGGTACCTG	240
61	<u>S V S P W</u> A Y R <u>I S Y D P A R Y P</u> R Y L	80
	CD-VII	CD-I
241	CCTGAAGCCTACTGCCCTGTGCCGGGGCTGCCCTGACCGGGCTGTTCGGCGAGGAGGACGTG	300
81	P E A Y <u>C L C R G C</u> L T G L F G E E D V	100
	CD-II	
301	CGCTTCGCGAGCGCCCTGTCTACATGCCCACCGTCGTCTGCGCCGACCCCGCCTGC	360
101	R F R S A P V Y M P T <u>V V L R R T P</u> A C	120
	CD-III	
361	GCCGGCGGGCGTTCCGTCTACACGAGGCCTACGTCACCATCCCCGTGGGCTGCACCTGC	420
121	A G G R S V Y T E A Y V T <u>I P V G C T C</u>	140
	CD-IV	
	#	
421	GTCCCCGAGCCGAGAGAAGGACGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC	480
141	<u>V</u> P E P E K D A D S I N S S I D K Q G A	160
	CD-IV	
481	AAGTCCTGTGGGCCCCAACGACGCGCCCGCTGGCCCTGA	522
161	K L L L G P N D A P A G P	174

**Figure 9**  
**Interleukin-22 Polypeptide Analysis**

